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#19

TECH CENTER 1600/2900



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1600

1646

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/445,614B

DATE: 06/21/2002
TIME: 14:07:36

Input Set : A:\T1481.txt
Output Set: N:\CRF3\06212002\I445614B.raw

4 <110> APPLICANT: Bonnert, Timothy Peter
6 <120> TITLE OF INVENTION: HUMAN VANILLOID RECEPTOR-LIKE RECEPTOR
9 <130> FILE REFERENCE: T1481
11 <140> CURRENT APPLICATION NUMBER: 09/445,614B
12 <141> CURRENT FILING DATE: 1999-12-08
14 <150> PRIOR APPLICATION NUMBER: 9827016.8
15 <151> PRIOR FILING DATE: 1998-12-08
17 <160> NUMBER OF SEQ ID NOS: 19
19 <170> SOFTWARE: FastSEQ for Windows Version 4.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 2469
23 <212> TYPE: DNA
24 <213> ORGANISM: Homo sapiens
26 <400> SEQUENCE: 1

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28	ggtcctggct ggaccgagca gcctcctcct cctaggatga cctcaccctc cagctctcca	120
29	gttttcaggt tggagacatt agatggaggg caagaagatg gctctgaggc ggacagagga	180
30	aagctggatt ttgggagcgg gctgcctccc atggagtcac agttccaggg cgaggaccgg	240
31	aaattcggcc ctcagataag agtcaacctc aactaccgaa agggAACAGG tgccagtca	300
32	ccggatccaa accgattga ccgagatcgg ctcttcaatg cggctctcccg ggggttcccc	360
33	gaggatctgg ctggacttcc agagtacctg agcaagacca gcaagtaccc caccgactcg	420
34	gaatacacag agggctccac aggttaagacg tgcctgtatga aggctgtgtc gaaccttaag	480
35	gacggagtca atgcctgcat tctgcccactg ctgcagatcg acaggggactc tggcaatcct	540
36	cagccccctgg taaatggccca gtgcacagat gactattacc gaggccacag cgctctgcac	600
37	atgccttattg agaagaggag tctgcagtgt gtgaagctcc tgggtggagaa tggggccaat	660
38	gtgcatttccc gggcctcgcc ccgttcttc cagaaggggcc aaggggactt cttttatttc	720
39	ggtgagctac ccctcttcc gggcgttgc accaagcagt gggatgttgt aagctaccc	780
40	ctggagaacc cacaccagcc cggcagcctg caggccactg actccccaggc caacacagtc	840
41	ctgcatttccc tagtgcgtat ctcggacaac tcagctgaga acattgcact ggtgaccagc	900
42	atgtatgtat ggctcttcca agctggggcc cgcctctgcc ctaccgtgca gcttgaggac	960
43	atccgcaacc tgcaggatct cacgcctctg aagctggccg ccaaggaggc caagatcgag	1020
44	attttcaggc acatcttgcg gccccggatggg tcaggactga gccacccttc cggaaagtcc	1080
45	accggatgggt gctatggcc tggccgggtg tcgcgtatg acctggcttc tggacagc	1140
46	tgtgaggaga actcagttgtc ggagatcatt gccttcatt gcaagagccc gcaccgacac	1200
47	cgaatggtcg ttttggagcc cctgaacaaa ctgctgcagg cgaaatggga tctgctcatc	1260
48	cccaaggatct tcttaaactt cctgtgtat ctgatctaca tggatctt caccgctgtt	1320
49	gcctaccatc agcctaccct gaagaagcag gcccggccctc acctgaaagc ggagggttgg	1380
50	aactccatgc tgctgacggg ccacatcctt atcctgtctg gggggatcta cctcctcg	1440
51	ggccatgtgt ggtacttctg gggccggccac gtgttcatct ggatctgtt catagacagc	1500
52	tactttgaaa tcctcttccct gttccaggcc ctgcacag tgggtgtccca ggtgtgtgt	1560
53	ttcctggcca tcgactggta cctgcccctg cttgtgtctg cgctgggtgt gggctggctg	1620
54	aacctgtttt actatacacg tggcttccag cacacaggca tctacagtgt catgtccag	1680
55	aaggatccatcc tgcgggaccc gctgcgttcc cttctgtatct acttagtctt cttttcgcc	1740

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56	ttcgctgttag	ccctggtag	cctgagccag	gaggcttggc	ccccgaagc	tcctacaggc	1800									
57	cccaatgcca	cagagtca	gcagccatg	gaggacagg	aggacgaggg	caacggggcc	1860									
58	cagtacaggg	gtatcctgga	aggctccttgc	gagctttca	aattcaccat	cggcatgggc	1920									
59	gagctggct	tccaggagca	gctgcacttc	cgcggcatgg	tgctgctgct	gctgctggcc	1980									
60	tacgctgtgc	tcacacctat	cctgctgtc	aacatgtca	tcgcccctcat	gagcgagacc	2040									
61	gtcaacagt	tcgcccactga	cagctggagc	atctgaaagc	tgcagaaagc	catctctgtc	2100									
62	ctggagatgg	agaatggcta	ttgggtggtc	aggaagaagc	agcggggcagg	tgtgatgctg	2160									
63	accgtggca	ctaagccaga	tggcagcccg	gatgagcgt	ggtgcttcag	ggtggaggag	2220									
64	gtgaactggg	cttcatggga	gcagacgctg	cctacgtgt	gtgaggacc	gtcaggggca	2280									
65	ggtgtccctc	gaactctcga	gaaccctgtc	ctggcttccc	ctcccaaggaa	ggatgaggat	2340									
66	ggtgcctctg	aggaaaacta	tgtgcccgtc	cagctcctcc	agtccaaactg	atggcccaaga	2400									
67	tgcagcagga	ggccagagga	cagagcagag	gatcttcca	accacatctg	ctggctctgg	2460									
68	ggtcccaagt						2469									
70	<210> SEQ ID NO: 2															
71	<211> LENGTH: 764															
72	<212> TYPE: PRT															
73	<213> ORGANISM: Homo sapiens															
75	<400> SEQUENCE: 2															
76	Met	Thr	Ser	Pro	Ser	Ser	Phe	Arg	Ile	Glu	Thr	Ile	Asp			
77	1				5			10			15					
78	Gly	Gly	Gln	Glu	Asp	Gly	Ser	Glu	Ala	Asp	Arg	Gly	Lys	Ile	Asp	Phe
79							20			25			30			
80	Gly	Ser	Gly	Leu	Pro	Pro	Met	Glu	Ser	Gln	Phe	Gln	Gly	Glu	Asp	Arg
81							35			40			45			
82	Lys	Phe	Ala	Pro	Gln	Ile	Arg	Val	Asn	Leu	Asn	Tyr	Arg	Lys	Gly	Thr
83							50			55			60			
84	Gly	Ala	Ser	Gln	Pro	Asp	Pro	Asn	Arg	Phe	Asp	Arg	Asp	Arg	Leu	Phe
85							65			70			75			80
86	Asn	Ala	Val	Ser	Arg	Gly	Val	Pro	Glu	Asp	Leu	Ala	Gly	Leu	Pro	Glu
87							85			90			95			
88	Tyr	Leu	Ser	Lys	Thr	Ser	Lys	Tyr	Leu	Thr	Asp	Ser	Glu	Tyr	Thr	Glu
89							100			105			110			
90	Gly	Ser	Thr	Gly	Lys	Thr	Cys	Leu	Met	Lys	Ala	Val	Leu	Asn	Leu	Lys
91							115			120			125			
92	Asp	Gly	Val	Asn	Ala	Cys	Ile	Leu	Pro	Leu	Leu	Gln	Ile	Asp	Arg	Asp
93							130			135			140			
94	Ser	Gly	Asn	Pro	Gln	Pro	Leu	Val	Asn	Ala	Gln	Cys	Thr	Asp	Asp	Tyr
95	145						145			150			155			160
96	Tyr	Arg	Gly	His	Ser	Ala	Leu	His	Ile	Ala	Ile	Glu	Lys	Arg	Ser	Leu
97							165			170			175			
98	Gln	Cys	Val	Lys	Leu	Leu	Val	Glu	Asn	Gly	Ala	Asn	Val	His	Ala	Arg
99							180			185			190			
100	Ala	Cys	Gly	Arg	Phe	Phe	Gln	Lys	Gly	Gly	Thr	Cys	Phe	Tyr	Phe	
101							195			200			205			
102	Gly	Glu	Leu	Pro	Leu	Ser	Leu	Ala	Ala	Cys	Thr	Lys	Gln	Trp	Asp	Val
103							210			215			220			
104	Val	Ser	Tyr	Leu	Leu	Glu	Asn	Pro	His	Gln	Pro	Ala	Ser	Leu	Gln	Ala
105	225						225			230			235			240
106	Thr	Asp	Ser	Gln	Gly	Asn	Thr	Val	Leu	His	Ala	Leu	Val	Met	Ile	Ser

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107	245	250	255
108	Asp Asn Ser Ala Glu Asn Ile Ala Leu Val Thr Ser Met Tyr Asp Gly		
109	260	265	270
110	Leu Leu Gln Ala Gly Ala Arg Leu Cys Pro Thr Val Gln Leu Glu Asp		
111	275	280	285
112	Ile Arg Asn Leu Gln Asp Leu Thr Pro Leu Lys Leu Ala Ala Lys Glu		
113	290	295	300
114	Gly Lys Ile Glu Ile Phe Arg His Ile Leu Gln Arg Glu Phe Ser Gly		
115	305	310	315
116	320	Leu Ser His Leu Ser Arg Lys Phe Thr Glu Trp Cys Tyr Gly Pro Val	
117	325	330	335
118	Arg Val Ser Leu Tyr Asp Leu Ala Ser Val Asp Ser Cys Glu Glu Asn		
119	340	345	350
120	Ser Val Leu Glu Ile Ile Ala Phe His Cys Lys Ser Pro His Arg His		
121	355	360	365
122	Arg Met Val Val Leu Glu Pro Leu Asn Lys Leu Leu Gln Ala Lys Trp		
123	370	375	380
124	Asp Leu Leu Ile Pro Lys Phe Phe Leu Asn Phe Leu Cys Asn Leu Ile		
125	385	390	395
126	400	Tyr Met Phe Ile Phe Thr Ala Val Ala Tyr His Gln Pro Thr Leu Lys	
127	405	410	415
128	Lys Gln Ala Ala Pro His Leu Lys Ala Glu Val Gly Asn Ser Met Leu		
129	420	425	430
130	Leu Thr Gly His Ile Leu Ile Leu Leu Gly Gly Ile Tyr Leu Leu Val		
131	435	440	445
132	Gly Gln Leu Trp Tyr Phe Trp Arg Arg His Val Phe Ile Trp Ile Ser		
133	450	455	460
134	Phe Ile Asp Ser Tyr Phe Glu Ile Leu Phe Leu Phe Gln Ala Leu Leu		
135	465	470	475
136	480	Thr Val Val Ser Gln Val Leu Cys Phe Leu Ala Ile Glu Trp Tyr Leu	
137	485	490	495
138	500	Pro Leu Leu Val Ser Ala Leu Val Leu Gly Trp Leu Asn Leu Leu Tyr	
139	505	510	
140	Tyr Thr Arg Gly Phe Gln His Thr Gly Ile Tyr Ser Val Met Ile Gln		
141	515	520	525
142	Lys Val Ile Leu Arg Asp Leu Leu Arg Phe Leu Leu Ile Tyr Leu Val		
143	530	535	540
144	Phe Leu Phe Gly Phe Ala Val Ala Leu Val Ser Leu Ser Gln Glu Ala		
145	545	550	555
146	560	Trp Arg Pro Glu Ala Pro Thr Gly Pro Asn Ala Thr Glu Ser Val Gln	
147	565	570	575
148	580	Pro Met Glu Gly Gln Glu Asp Glu Gly Asn Gly Ala Gln Tyr Arg Gly	
149	585	590	
150	Ile Leu Glu Ala Ser Leu Glu Leu Phe Lys Phe Thr Ile Gly Met Gly		
151	595	600	605
152	Glu Leu Ala Phe Gln Glu Gln Leu His Phe Arg Gly Met Val Leu Leu		
153	610	615	620
154	Leu Leu Leu Ala Tyr Val Leu Leu Thr Tyr Ile Leu Leu Leu Asn Met		
155	625	630	635
			640

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156 Leu Ile Ala Leu Met Ser Glu Thr Val Asn Ser Val Ala Thr Asp Ser
 157 645 650 655
 158 Trp Ser Ile Trp Lys Leu Gln Lys Ala Ile Ser Val Leu Glu Met Glu
 159 660 665 670
 160 Asn Gly Tyr Trp Trp Cys Arg Lys Lys Gln Arg Ala Gly Val Met Leu
 161 675 680 685
 162 Thr Val Gly Thr Lys Pro Asp Gly Ser Pro Asp Glu Arg Trp Cys Phe
 163 690 695 700
 164 Arg Val Glu Glu Val Asn Trp Ala Ser Trp Glu Gln Thr Leu Pro Thr
 165 705 710 715 720
 166 Leu Cys Glu Asp Pro Ser Gly Ala Gly Val Pro Arg Thr Leu Glu Asn
 167 725 730 735
 168 Pro Val Leu Ala Ser Pro Pro Lys Glu Asp Glu Asp Gly Ala Ser Glu
 169 740 745 750
 170 Glu Asn Tyr Val Pro Val Gln Leu Leu Gln Ser Asn
 171 755 760
 173 <210> SEQ ID NO: 3
 174 <211> LENGTH: 51
 175 <212> TYPE: DNA
 176 <213> ORGANISM: Artificial Sequence
 178 <220> FEATURE:
 179 <223> OTHER INFORMATION: Primer
 181 <400> SEQUENCE: 3
 182 tgttaccaat ctgaagtggg agcggccggc tcattttttt ttttttttt t 51
 184 <210> SEQ ID NO: 4
 185 <211> LENGTH: 21
 186 <212> TYPE: DNA
 187 <213> ORGANISM: Artificial Sequence
 189 <220> FEATURE:
 190 <223> OTHER INFORMATION: PCR Primer
 192 <400> SEQUENCE: 4
 193 caggccccggg catgcacatt g 21
 195 <210> SEQ ID NO: 5
 196 <211> LENGTH: 21
 197 <212> TYPE: DNA
 198 <213> ORGANISM: Artificial Sequence
 200 <220> FEATURE:
 201 <223> OTHER INFORMATION: PCR Primer
 203 <400> SEQUENCE: 5
 204 ccagggcgag gaccggaaat t 21
 206 <210> SEQ ID NO: 6
 207 <211> LENGTH: 21
 208 <212> TYPE: DNA
 209 <213> ORGANISM: Artificial Sequence
 211 <220> FEATURE:
 212 <223> OTHER INFORMATION: PCR Primer
 214 <400> SEQUENCE: 6
 215 gacagctgga gcatctggaa g 21
 217 <210> SEQ ID NO: 7

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218 <211> LENGTH: 21
219 <212> TYPE: DNA
220 <213> ORGANISM: Artificial Sequence
222 <220> FEATURE:
223 <223> OTHER INFORMATION: PCR Primer
225 <400> SEQUENCE: 7
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228 <210> SEQ ID NO: 8
229 <211> LENGTH: 21
230 <212> TYPE: DNA
231 <213> ORGANISM: Artificial Sequence
233 <220> FEATURE:
234 <223> OTHER INFORMATION: PCR Primer
236 <400> SEQUENCE: 8
237 ctccagatg ctccagctgt c 21
239 <210> SEQ ID NO: 9
240 <211> LENGTH: 21
241 <212> TYPE: DNA
242 <213> ORGANISM: Artificial Sequence
244 <220> FEATURE:
245 <223> OTHER INFORMATION: PCR Primer
247 <400> SEQUENCE: 9
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250 <210> SEQ ID NO: 10
251 <211> LENGTH: 21
252 <212> TYPE: DNA
253 <213> ORGANISM: Artificial Sequence
255 <220> FEATURE:
256 <223> OTHER INFORMATION: PCR Primer
258 <400> SEQUENCE: 10
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261 <210> SEQ ID NO: 11
262 <211> LENGTH: 21
263 <212> TYPE: DNA
264 <213> ORGANISM: Artificial Sequence
266 <220> FEATURE:
267 <223> OTHER INFORMATION: PCR Primer
269 <400> SEQUENCE: 11
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272 <210> SEQ ID NO: 12
273 <211> LENGTH: 21
274 <212> TYPE: DNA
275 <213> ORGANISM: Artificial Sequence
277 <220> FEATURE:
278 <223> OTHER INFORMATION: PCR Primer
280 <400> SEQUENCE: 12
281 gccctaccgt gcagcttgag g 21
283 <210> SEQ ID NO: 13
284 <211> LENGTH: 21

VERIFICATION SUMMARY DATE: 06/21/2002
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